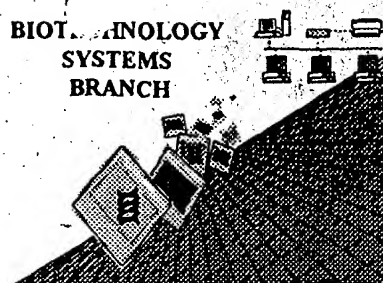


*J. Weber*

## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/483,543

Source: 1651

Date Processed by STIC: 5-14-01

RECEIVED

MAY 30 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

BEST AVAILABLE COPY

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/483,543

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

RECEIVED

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- 1 ☐ Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES)      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES)      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10 ☐ Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of "Artificial" (NEW RULES)      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
Valid response is Artificial Sequence.
- 12 ☒ Use of <220>Feature (NEW RULES)      Sequence(s)        are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

#11

Does Not Comply  
Corrected Diskette Needed  
see p. 2

DATE: 05/14/2001

TIME: 11:53:46

Output Set: N:\CRF3\05142001\I483543.raw

60  
64

RAW SEQUENCE LISTING                      DATE: 05/14/2001  
 PATENT APPLICATION: US/09/483,543        TIME: 11:53:46

Input Set : A:\Sequence Listing.txt  
 Output Set: N:\CRF3\05142001\I483543.raw

78 <212> TYPE: PRT  
 79 <213> ORGANISM: Artificial Sequence  
 81 <220> FEATURE:  
 82 <223> OTHER INFORMATION: Unsure → what is the source of the  
 84 <400> SEQUENCE: 5                      genetic material in the sequence?  
 85 Met Ala Ser Ser Arg Val Asp Gly Gly Arg Ser Asp Leu Ile Glu Gly    See #12 on the  
 86    1                      5                      10                      15                      Error Summary Sheet.  
 87 Arg Cys  
 90 <210> SEQ ID NO: 6  
 91 <211> LENGTH: 18  
 92 <212> TYPE: PRT  
 93 <213> ORGANISM: Artificial Sequence  
 95 <220> FEATURE:  
 96 <223> OTHER INFORMATION: Cys-F1-PS-Biotin Construct  
 98 <220> FEATURE:  
 99 <221> NAME/KEY: misc\_feature  
 100 <222> LOCATION: 3  
 101 <223> OTHER INFORMATION: Xaa = Lys-[Dapa(F1)]  
 103 <220> FEATURE:  
 104 <221> NAME/KEY: misc\_feature  
 105 <222> LOCATION: 17  
 106 <223> OTHER INFORMATION: Xaa = [Lys-(Biotin)]  
 108 <400> SEQUENCE: 6  
 W--> 109 Cys Gly Xaa Gly Leu Glu Val Leu Phe Gln Gly Pro Val Arg Lys Gly  
 110    1                      5                      10                      15  
 W--> 111 Xaa Gly  
 114 <210> SEQ ID NO: 7  
 115 <211> LENGTH: 11  
 116 <212> TYPE: PRT  
 117 <213> ORGANISM: Artificial Sequence  
 119 <220> FEATURE:  
 120 <223> OTHER INFORMATION: High affinity ligand for the N-SH3 Domain of Crk  
 122 <400> SEQUENCE: 7  
 123 Pro Pro Pro Ala Leu Pro Pro Lys Arg Arg Arg  
 124    1                      5                      10  
 127 <210> SEQ ID NO: 8  
 128 <211> LENGTH: 318  
 129 <212> TYPE: PRT  
 130 <213> ORGANISM: Artificial Sequence  
 132 <220> FEATURE:  
 133 <223> OTHER INFORMATION: Protein Kinase Target  
 135 <220> FEATURE:  
 136 <221> NAME/KEY: misc\_feature  
 137 <222> LOCATION: 311  
 138 <223> OTHER INFORMATION: Xaa = Lys-[Dapa(F1)]  
 140 <400> SEQUENCE: 8  
 141 Lys Arg Gly Cys Ala Gly Asn Phe Asp Ser Glu Glu Arg Ser Ser Trp  
 142    1                      5                      10                      15  
 143 Tyr Trp Gly Arg Leu Ser Arg Gln Glu Ala Val Ala Leu Leu Gln Gly

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/483,543

DATE: 05/14/2001  
TIME: 11:53:46

Input Set : A:\Sequence Listing.txt  
Output Set: N:\CRF3\05142001\I483543.raw

```

144          20          25          30
145 Gln Arg His Gly Val Phe Leu Val Arg Asp Ser Ser Thr Ser Pro Gly
146          35          40          45
147 Asp Tyr Val Leu Ser Val Ser Glu Asn Ser Arg Val Ser His Tyr Ile
148          50          55          60
149 Ile Asn Ser Ser Gly Pro Arg Pro Pro Val Pro Pro Ser Pro Ala Gln
150          65          70          75          80
151 Pro Pro Pro Gly Val Ser Pro Ser Arg Leu Arg Ile Gly Asp Gln Glu
152          85          90          95
153 Phe Asp Ser Leu Pro Ala Leu Leu Glu Phe Tyr Lys Ile His Tyr Leu
154          100          105          110
155 Asp Thr Thr Thr Leu Ile Glu Pro Val Ala Arg Ser Arg Gln Gly Ser
156          115          120          125
157 Gly Val Ile Leu Arg Gln Glu Glu Ala Glu Tyr Val Arg Ala Leu Phe
158          130          135          140
159 Asp Phe Asn Gly Asn Asp Glu Glu Asp Leu Pro Phe Lys Lys Gly Asp
160          145          150          155          160
161 Ile Leu Arg Ile Arg Asp Lys Pro Glu Glu Gln Trp Trp Asn Ala Glu
162          165          170          175
163 Asp Ser Glu Gly Lys Arg Gly Met Ile Pro Val Pro Tyr Val Glu Lys
164          180          185          190
165 Tyr Arg Pro Ala Ser Ala Ser Val Ser Ala Leu Ile Gly Gly Asn Gln
166          195          200          205
167 Glu Gly Ser His Pro Gln Pro Leu Gly Gly Pro Glu Pro Gly Pro Tyr
168          210          215          220
169 Ala Gln Pro Ser Val Asn Thr Pro Leu Pro Asn Leu Gln Asn Gly Pro
170          225          230          235          240
171 Ile Tyr Ala Arg Val Ile Gln Lys Arg Val Pro Asn Ala Tyr Asp Lys
172          245          250          255
173 Thr Ala Leu Ala Leu Glu Val Gly Glu Leu Val Lys Val Thr Lys Ile
174          260          265          270
175 Asn Val Ser Gly Gln Trp Glu Gly Cys Asn Gly Lys Arg Gly His
176          275          280          285
177 Phe Pro Phe Thr His Val Arg Leu Leu Asp Gln Gln Asn Pro Asp Glu
178          290          295          300
W--> 179 Asp Phe Ser Gly Cys Gly Xaa Gly Leu Glu Val Leu Phe Gln
180          305          310          315
190 <210> SEQ ID NO: 9
191 <211> LENGTH: 326
192 <212> TYPE: PRT
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
196 <223> OTHER INFORMATION: Recombinant Intermediate
198 <220> FEATURE:
199 <221> NAME/KEY: misc_feature
200 <222> LOCATION: 311
201 <223> OTHER INFORMATION: Xaa = Lys-[Dapa(Fl)]
203 <220> FEATURE:
204 <221> NAME/KEY: misc_feature

```

## RAW SEQUENCE LISTING

DATE: 05/14/2001

PATENT APPLICATION: US/09/483,543

TIME: 11:53:46

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\05142001\I483543.raw

```

205 <222> LOCATION: 325
206 <223> OTHER INFORMATION: Xaa = [Lys-(Biotin)]
208 <400> SEQUENCE: 9
209 Lys Arg Gly Cys Ala Gly Asn Phe Asp Ser Glu Glu Arg Ser Ser Trp
210 1 5 10 15
211 Tyr Trp Gly Arg Leu Ser Arg Gln Glu Ala Val Ala Leu Leu Gln Gly
212 20 25 30
213 Gln Arg His Gly Val Phe Leu Val Arg Asp Ser Ser Thr Ser Pro Gly
214 35 40 45
215 Asp Tyr Val Leu Ser Val Ser Glu Asn Ser Arg Val Ser His Tyr Ile
216 50 55 60
217 Ile Asn Ser Ser Gly Pro Arg Pro Pro Val Pro Pro Ser Pro Ala Gln
218 65 70 75 80
219 Pro Pro Pro Gly Val Ser Pro Ser Arg Leu Arg Ile Gly Asp Gln Glu
220 85 90 95
221 Phe Asp Ser Leu Pro Ala Leu Leu Glu Phe Tyr Lys Ile His Tyr Leu
222 100 105 110
223 Asp Thr Thr Thr Leu Ile Glu Pro Val Ala Arg Ser Arg Gln Gly Ser
224 115 120 125
225 Gly Val Ile Leu Arg Gln Glu Glu Ala Glu Tyr Val Arg Ala Leu Phe
226 130 135 140
227 Asp Phe Asn Gly Asn Asp Glu Glu Asp Leu Pro Phe Lys Lys Gly Asp
228 145 150 155 160
229 Ile Leu Arg Ile Arg Asp Lys Pro Glu Glu Gln Trp Trp Asn Ala Glu
230 165 170 175
231 Asp Ser Glu Gly Lys Arg Gly Met Ile Pro Val Pro Tyr Val Glu Lys
232 180 185 190
233 Tyr Arg Pro Ala Ser Ala Ser Val Ser Ala Leu Ile Gly Gly Asn Gln
234 195 200 205
235 Glu Gly Ser His Pro Gln Pro Leu Gly Gly Pro Glu Pro Gly Pro Tyr
236 210 215 220
237 Ala Gln Pro Ser Val Asn Thr Pro Leu Pro Asn Leu Gln Asn Gly Pro
238 225 230 235 240
239 Ile Tyr Ala Arg Val Ile Gln Lys Arg Val Pro Asn Ala Tyr Asp Lys
240 245 250 255
241 Thr Ala Leu Ala Leu Glu Val Gly Glu Leu Val Lys Val Thr Lys Ile
242 260 265 270
243 Asn Val Ser Gly Gln Trp Glu Gly Glu Cys Asn Gly Lys Arg Gly His
244 275 280 285
245 Phe Pro Phe Thr His Val Arg Leu Leu Asp Gln Gln Asn Pro Asp Glu
246 290 295 300
W--> 247 Asp Phe Ser Gly Cys Gly Xaa Gly Leu Glu Val Leu Phe Gln Gly Pro
248 305 310 315 320
W--> 249 Val Arg Lys Gly Xaa Gly
250 325

```

## VERIFICATION SUMMARY

DATE: 05/14/2001

PATENT APPLICATION: US/09/483,543

TIME: 11:53:47

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF3\05142001\I483543.raw

L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9